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OM protein - protein search, using sw model

Run on: February 11, 2005, 11:53:58 ; Search time 374 Seconds
(without alignments)
101.345 Million cell updates/sec

Title: US-09-824-134-2_COPY_130_245

Perfect score: 593
Sequence: 1 FEAGAAAGAPGEDLCAAF.....QEYQARDLQNRSGAMSPMS 116

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1376875 seqs, 326749119 residues

Total number of hits satisfying chosen parameters: 1376875

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA:*

1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep.*
2: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep.*
3: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep.*
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10: /cgn2_6/ptodata/1/pubpaa/US09B_PUBCOMB.pep.*
11: /cgn2_6/ptodata/1/pubpaa/US09C_PUBCOMB.pep.*
12: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep.*
13: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep.*
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15: /cgn2_6/ptodata/1/pubpaa/US10C_PUBCOMB.pep.*
16: /cgn2_6/ptodata/1/pubpaa/US10D_PUBCOMB.pep.*
17: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep.*
18: /cgn2_6/ptodata/1/pubpaa/US11_NEW_PUB.pep.*
19: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep.*
20: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	593	100.0	208	14	US-10-207-655-184
2	593	100.0	208	14	US-10-207-655-190
3	593	100.0	211	14	US-10-207-655-408
4	593	100.0	256	9	US-09-933-814-2
5	593	100.0	256	9	US-09-824-134-2
6	593	100.0	256	15	US-10-368-438-2
7	593	100.0	256	17	US-10-923-031-2
8	382.5	64.5	210	14	US-10-207-655-418
9	382	64.4	74	13	US-10-112-793-25
10	382	64.4	74	14	US-10-287-594-5
11	318	53.6	62	13	US-10-035-408-5
12	143.5	24.2	95	11	US-09-972-211-128
13	143.5	24.2	95	15	US-10-087-684-87

14	143.5	24.2	95	15	US-10-218-779-87	Sequence 87, Appl
15	143.5	24.2	95	15	US-10-096-625-128	Sequence 128, App
16	143.5	24.2	96	10	US-09-970-944-45	Sequence 45, Appl
17	143.5	24.2	96	15	US-10-037-417-124	Sequence 124, App
18	131	22.1	82	15	US-10-087-684-89	Sequence 89, Appl
19	131	22.1	82	15	US-10-218-779-89	Sequence 89, Appl
20	131	22.1	83	10	US-09-970-944-47	Sequence 47, Appl
21	131	22.1	83	15	US-10-037-417-126	Sequence 126, App
22	115.5	19.5	656	9	US-09-862-027-30	Sequence 30, Appl
23	111.5	18.8	77	14	US-10-287-594-7	Sequence 7, Appl
24	111.5	18.8	99	15	US-10-359-439-3	Sequence 3, Appl
25	111.5	18.8	100	15	US-10-359-439-1	Sequence 1, Appl
26	111.5	18.8	273	15	US-10-108-260A-3780	Sequence 3780, Ap
27	111.5	18.8	671	9	US-09-758-003-2	Sequence 2, Appl
28	111.5	18.8	671	9	US-09-862-027-29	Sequence 29, Appl
29	111.5	18.8	671	10	US-09-981-397A-16	Sequence 16, Appl
30	111.5	18.8	671	16	US-10-408-765A-2254	Sequence 2254, Ap
31	108.5	18.3	77	13	US-10-112-793-27	Sequence 27, Appl
32	96.5	16.3	396	14	US-10-336-031-1	Sequence 1, Appl
33	86	14.5	294	14	US-10-336-031-2	Sequence 2, Appl
34	86	14.5	400	15	US-10-104-047-2995	Sequence 2995, Ap
35	86	14.5	1762	14	US-10-205-194-117	Sequence 117, App
36	86	14.5	3913	15	US-10-334-143-45	Sequence 45, Appl
37	83	14.0	657	14	US-10-186-185-2	Sequence 2, Appl
38	81	13.7	63	13	US-10-035-408-2	Sequence 2, Appl
39	81	13.7	81	14	US-10-287-594-6	Sequence 6, Appl
40	81	13.7	312	14	US-10-207-655-186	Sequence 186, App
41	81	13.7	328	15	US-10-296-115-1123	Sequence 1123, Ap
42	79.5	13.4	157	14	US-10-193-934-11	Sequence 11, Appl
43	78.5	13.2	1585	16	US-10-437-963-124349	Sequence 124349
44	78	13.2	104	14	US-10-029-386-30750	Sequence 30750, A
45	78	13.2	199	14	US-10-287-594-2	Sequence 2, Appl

ALIGNMENTS

RESULT 1

US-10-207-655-184
; Sequence 184, Application US/10207655
; Publication No. US20030118592A1
; GENERAL INFORMATION:
; APPLICANT: Ledbetter, Jeffrey A.
; APPLICANT: Hayden-Ledbetter, Martha S.
; TITLE OF INVENTION: BINDING DOMAIN-IMMUNOGLOBULIN FUSION PROTEINS
; FILE REFERENCE: 390069.401C1
; CURRENT APPLICATION NUMBER: US/10/207,655
; CURRENT FILING DATE: 2002-07-25
; NUMBER OF SEQ ID NOS: 426
; SOFTWARE: Patentin version 3.0
; SEQ ID NO 184
; LENGTH: 208
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-207-655-184

Query Match 100.0%; Score 593; DB 14; Length 208;
Best Local Similarity 100.0%; Pred. No. 4e-59;
Matches 116; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	FEAGAAAGAPGEDLCAAFNVICDNVGDWRRLAROLKVSDTKIDSIEDYPRNLTRV	60
Db	82	FEAGAAAGAPGEDLCAAFNVICDNVGDWRRLAROLKVSDTKIDSIEDYPRNLTRV	141
Qy	61	RESLRITWNTKENATVAHLVGLRSCNNLVADLVQVQOARDLQNRSGAMSPMS	116
Db	142	RESLRITWNTKENATVAHLVGLRSCNNLVADLVQVQOARDLQNRSGAMSPMS	197

RESULT 2

US-10-207-655-190
; Sequence 190, Application US/10207655
; Publication No. US20030118592A1

GENERAL INFORMATION:
APPLICANT: Ledbetter, Jeffrey A.
TITLE OF INVENTION: BINDING DOMAIN-IMMUNOGLOBULIN FUSION PROTEINS
FILE REFERENCE: 390069.401C1
CURRENT APPLICATION NUMBER: US/10/207,655
CURRENT FILING DATE: 2002-07-25
NUMBER OF SEQ ID NOS: 426
SOFTWARE: PatentIn version 3.0
SEQ ID NO 190
LENGTH: 208
TYPE: PRT
ORGANISM: Homo sapiens
US-10-207-655-190

Query Match 100.0%; Score 593; DB 14; Length 208;
Best Local Similarity 100.0%; Pred. No. 4e-59;
Matches 116; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FEAGAAAGAAAGGEEEDLCAAFNVICDNVGVKDWRRRLARQLKVSPTKIDSIEDRYPRNLTERV 60
DB 82 FEAGAAAGAAAGGEEEDLCAAFNVICDNVGVKDWRRRLARQLKVSPTKIDSIEDRYPRNLTERV 141
QY 61 RESLRWKTEKENATVAHLVGLALRSQCNMLVADLVQEVQQAARDLQNRSGAMSPMS 116
DB 142 RESLRWKTEKENATVAHLVGLALRSQCNMLVADLVQEVQQAARDLQNRSGAMSPMS 197

RESULT 3
US-10-207-655-408
Sequence 408, Application US/10207655
Publication No. US20030118592A1
GENERAL INFORMATION:
APPLICANT: Ledbetter, Jeffrey A.
TITLE OF INVENTION: BINDING DOMAIN-IMMUNOGLOBULIN FUSION PROTEINS
FILE REFERENCE: 390069.401C1
CURRENT APPLICATION NUMBER: US/10/207,655
CURRENT FILING DATE: 2002-07-25
NUMBER OF SEQ ID NOS: 426
SOFTWARE: PatentIn version 3.0
SEQ ID NO 408
LENGTH: 211
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: fusion polypeptide
US-10-207-655-408

Query Match 100.0%; Score 593; DB 14; Length 211;
Best Local Similarity 100.0%; Pred. No. 4.1e-59;
Matches 116; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FEAGAAAGAAAGGEEEDLCAAFNVICDNVGVKDWRRRLARQLKVSPTKIDSIEDRYPRNLTERV 60
DB 85 FEAGAAAGAAAGGEEEDLCAAFNVICDNVGVKDWRRRLARQLKVSPTKIDSIEDRYPRNLTERV 144
QY 61 RESLRWKTEKENATVAHLVGLALRSQCNMLVADLVQEVQQAARDLQNRSGAMSPMS 116
DB 145 RESLRWKTEKENATVAHLVGLALRSQCNMLVADLVQEVQQAARDLQNRSGAMSPMS 200

RESULT 4
US-09-933-814-2
Sequence 2, Application US/09933814
Patent No. US20020058798A1
GENERAL INFORMATION:
APPLICANT: Ledbetter, Jeffrey A.
TITLE OF INVENTION: BINDING DOMAIN-IMMUNOGLOBULIN FUSION PROTEINS
FILE REFERENCE: 390069.401C1
CURRENT APPLICATION NUMBER: US/10/207,655
CURRENT FILING DATE: 2002-07-25
NUMBER OF SEQ ID NOS: 426
SOFTWARE: PatentIn version 3.0
SEQ ID NO 190
LENGTH: 208
TYPE: PRT
ORGANISM: Homo sapiens
US-09-933-814-2

Query Match 100.0%; Score 593; DB 9; Length 256;
Best Local Similarity 100.0%; Pred. No. 5.2e-59;
Matches 116; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FEAGAAAGAAAGGEEEDLCAAFNVICDNVGVKDWRRRLARQLKVSPTKIDSIEDRYPRNLTERV 60
DB 130 FEAGAAAGAAAGGEEEDLCAAFNVICDNVGVKDWRRRLARQLKVSPTKIDSIEDRYPRNLTERV 189
QY 61 RESLRWKTEKENATVAHLVGLALRSQCNMLVADLVQEVQQAARDLQNRSGAMSPMS 116
DB 190 RESLRWKTEKENATVAHLVGLALRSQCNMLVADLVQEVQQAARDLQNRSGAMSPMS 245

RESULT 5
US-09-824-134-2
Sequence 2, Application US/09824134
Patent No. US20020082401A1
GENERAL INFORMATION:
APPLICANT: WALLACH, David
BOLDIN, Mark
VARFOLOMEV, Eugene
METT, Igor
TITLE OF INVENTION: MODULATORS OF THE FUNCTION OF FAS/APO1
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESS: BROWDY AND NEIMARK, P.L.L.C.
STREET: 419 Seventh Street N.W., Ste. 300
CITY: Washington
STATE: D.C.
COUNTRY: United States of America
ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/824,134
FILING DATE: 03-Apr-2001
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/860,082
FILING DATE: <Unknown>
APPLICATION NUMBER: IL 112022
FILING DATE: 15-DEC-1994
APPLICATION NUMBER: IL 112692
FILING DATE: 19-FEB-1995
APPLICATION NUMBER: IL 114615
FILING DATE: 16-JUL-1995
ATTORNEY/AGENT INFORMATION:
NAME: BROWDY, Roger L.
REGISTRATION NUMBER: 25,618
REFERENCE/DOCKET NUMBER: WALLACH=16
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 628-5197

GENERAL INFORMATION:
APPLICANT: Ledbetter, Jeffrey A.
TITLE OF INVENTION: BINDING DOMAIN-IMMUNOGLOBULIN FUSION PROTEINS
FILE REFERENCE: 390069.401C1
CURRENT APPLICATION NUMBER: US/10/207,655
CURRENT FILING DATE: 2002-07-25
NUMBER OF SEQ ID NOS: 426
SOFTWARE: PatentIn version 3.0
SEQ ID NO 190
LENGTH: 208
TYPE: PRT
ORGANISM: Homo sapiens
US-10-207-655-190

Query Match 100.0%; Score 593; DB 14; Length 208;
Best Local Similarity 100.0%; Pred. No. 4e-59;
Matches 116; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FEAGAAAGAAAGGEEEDLCAAFNVICDNVGVKDWRRRLARQLKVSPTKIDSIEDRYPRNLTERV 60
DB 82 FEAGAAAGAAAGGEEEDLCAAFNVICDNVGVKDWRRRLARQLKVSPTKIDSIEDRYPRNLTERV 141
QY 61 RESLRWKTEKENATVAHLVGLALRSQCNMLVADLVQEVQQAARDLQNRSGAMSPMS 116
DB 142 RESLRWKTEKENATVAHLVGLALRSQCNMLVADLVQEVQQAARDLQNRSGAMSPMS 197

RESULT 3
US-10-207-655-408
Sequence 408, Application US/10207655
Publication No. US20030118592A1
GENERAL INFORMATION:
APPLICANT: Ledbetter, Jeffrey A.
TITLE OF INVENTION: BINDING DOMAIN-IMMUNOGLOBULIN FUSION PROTEINS
FILE REFERENCE: 390069.401C1
CURRENT APPLICATION NUMBER: US/10/207,655
CURRENT FILING DATE: 2002-07-25
NUMBER OF SEQ ID NOS: 426
SOFTWARE: PatentIn version 3.0
SEQ ID NO 408
LENGTH: 211
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: fusion polypeptide
US-10-207-655-408

Query Match 100.0%; Score 593; DB 14; Length 211;
Best Local Similarity 100.0%; Pred. No. 4.1e-59;
Matches 116; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FEAGAAAGAAAGGEEEDLCAAFNVICDNVGVKDWRRRLARQLKVSPTKIDSIEDRYPRNLTERV 60
DB 85 FEAGAAAGAAAGGEEEDLCAAFNVICDNVGVKDWRRRLARQLKVSPTKIDSIEDRYPRNLTERV 144
QY 61 RESLRWKTEKENATVAHLVGLALRSQCNMLVADLVQEVQQAARDLQNRSGAMSPMS 116
DB 145 RESLRWKTEKENATVAHLVGLALRSQCNMLVADLVQEVQQAARDLQNRSGAMSPMS 200

RESULT 4
US-09-933-814-2
Sequence 2, Application US/09933814
Patent No. US20020058798A1
GENERAL INFORMATION:
APPLICANT: Ledbetter, Jeffrey A.
TITLE OF INVENTION: BINDING DOMAIN-IMMUNOGLOBULIN FUSION PROTEINS
FILE REFERENCE: 390069.401C1
CURRENT APPLICATION NUMBER: US/10/207,655
CURRENT FILING DATE: 2002-07-25
NUMBER OF SEQ ID NOS: 426
SOFTWARE: PatentIn version 3.0
SEQ ID NO 190
LENGTH: 208
TYPE: PRT
ORGANISM: Homo sapiens
US-09-933-814-2

Query Match 100.0%; Score 593; DB 9; Length 256;
Best Local Similarity 100.0%; Pred. No. 5.2e-59;
Matches 116; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FEAGAAAGAAAGGEEEDLCAAFNVICDNVGVKDWRRRLARQLKVSPTKIDSIEDRYPRNLTERV 60
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QY 61 RESLRWKTEKENATVAHLVGLALRSQCNMLVADLVQEVQQAARDLQNRSGAMSPMS 116
DB 190 RESLRWKTEKENATVAHLVGLALRSQCNMLVADLVQEVQQAARDLQNRSGAMSPMS 245

RESULT 5
US-09-824-134-2
Sequence 2, Application US/09824134
Patent No. US20020082401A1
GENERAL INFORMATION:
APPLICANT: WALLACH, David
BOLDIN, Mark
VARFOLOMEV, Eugene
METT, Igor
TITLE OF INVENTION: MODULATORS OF THE FUNCTION OF FAS/APO1
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESS: BROWDY AND NEIMARK, P.L.L.C.
STREET: 419 Seventh Street N.W., Ste. 300
CITY: Washington
STATE: D.C.
COUNTRY: United States of America
ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/824,134
FILING DATE: 03-Apr-2001
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/860,082
FILING DATE: <Unknown>
APPLICATION NUMBER: IL 112022
FILING DATE: 15-DEC-1994
APPLICATION NUMBER: IL 112692
FILING DATE: 19-FEB-1995
APPLICATION NUMBER: IL 114615
FILING DATE: 16-JUL-1995
ATTORNEY/AGENT INFORMATION:
NAME: BROWDY, Roger L.
REGISTRATION NUMBER: 25,618
REFERENCE/DOCKET NUMBER: WALLACH=16
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 628-5197

TELEFAX: (202) 737-3528
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 256 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-09-824-134-2

Query Match 100.0%; Score 593; DB 9; Length 256;
Best Local Similarity 100.0%; Pred. No. 5.2e-59;
Matches 116; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FEAGAAAGAAPEEDLCAAFNVICNVGKDWRLARQLKVSQTKIDSIEDRYPRNLTERV 60
DB 130 FEAGAAAGAAPEEDLCAAFNVICNVGKDWRLARQLKVSQTKIDSIEDRYPRNLTERV 189

QY 61 RESLRWKNTKENATVAHLVGLRSCQNNLVADLVQEVQQAARDLQNRSGAMSPMS 116
DB 190 RESLRWKNTKENATVAHLVGLRSCQNNLVADLVQEVQQAARDLQNRSGAMSPMS 245

RESULT 6
US-10-368-438-2
Sequence 2, Application US/10368438
Publication No. US20030219411A1
GENERAL INFORMATION:
APPLICANT: David WALLACH
Mark P. BOLDIN
Tanya M. GONCHAROV
Yury V. GOLTSEV
TITLE OF INVENTION: MODULATORS OF THE FUNCTION OF FAS RECEPTORS
AND OTHER PROTEINS
NUMBER OF SEQUENCES: 34
CORRESPONDENCE ADDRESS:
ADDRESS: Browdy and Neimark
STREET: 419 Seventh Street N.W., Ste. 300
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/368,438
FILING DATE: 20-Feb-2003
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/983,502
FILING DATE: 16-JAN-1998
APPLICATION NUMBER: PCT/US96/10521
FILING DATE: 14-JUN-1996
APPLICATION NUMBER: IL 114,615
FILING DATE: 16-JUL-1995
APPLICATION NUMBER: IL 114,986
FILING DATE: 17-AUG-1995
APPLICATION NUMBER: IL 115,319
FILING DATE: 14-SEP-1995
APPLICATION NUMBER: IL 116,588
FILING DATE: 27-DEC-1995
APPLICATION NUMBER: IL 117,932
FILING DATE: 16-APR-1996
ATTORNEY/AGENT INFORMATION:
NAME: Browdy, Roger L.
REGISTRATION NUMBER: 25,618
REFERENCE/DOCKET NUMBER: WALLACH-19
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 628-5197
TELEFAX: (202) 737-3528
INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:
LENGTH: 256 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-10-368-438-2

Query Match 100.0%; Score 593; DB 15; Length 256;
Best Local Similarity 100.0%; Pred. No. 5.2e-59;
Matches 116; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FEAGAAAGAAPEEDLCAAFNVICNVGKDWRLARQLKVSQTKIDSIEDRYPRNLTERV 60
DB 130 FEAGAAAGAAPEEDLCAAFNVICNVGKDWRLARQLKVSQTKIDSIEDRYPRNLTERV 189

QY 61 RESLRWKNTKENATVAHLVGLRSCQNNLVADLVQEVQQAARDLQNRSGAMSPMS 116
DB 190 RESLRWKNTKENATVAHLVGLRSCQNNLVADLVQEVQQAARDLQNRSGAMSPMS 245

RESULT 7
US-10-923-031-2
Sequence 2, Application US/10923031
Publication No. US20050013816A1
GENERAL INFORMATION:
APPLICANT: WALLACH, David
APPLICANT: BOLDIN, Mark
APPLICANT: VAREFOLOMEV, Eugene
APPLICANT: METT, Igor
TITLE OF INVENTION: MODULATORS OF THE FUNCTION OF FAS/APOL RECEPTORS
FILE REFERENCE: WALLACH-168
CURRENT APPLICATION NUMBER: US/10/923,031
CURRENT FILING DATE: 2004-08-23
PRIOR APPLICATION NUMBER: US/09/933,814
PRIOR FILING DATE: 2001-08-22
PRIOR APPLICATION NUMBER: 08/860,082
PRIOR FILING DATE: 1997-08-19
PRIOR APPLICATION NUMBER: PCT/US95/16542
PRIOR FILING DATE: 1995-12-14
PRIOR APPLICATION NUMBER: IL 112022
PRIOR FILING DATE: 1994-12-15
PRIOR APPLICATION NUMBER: IL 112692
PRIOR FILING DATE: 1995-02-19
NUMBER OF SEQ ID NOS: 2
SOFTWARE: Patent In version 3.0
SEQ ID NO 2
LENGTH: 256
TYPE: PRT
ORGANISM: Homo sapiens
US-10-923-031-2

Query Match 100.0%; Score 593; DB 17; Length 256;
Best Local Similarity 100.0%; Pred. No. 5.2e-59;
Matches 116; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FEAGAAAGAAPEEDLCAAFNVICNVGKDWRLARQLKVSQTKIDSIEDRYPRNLTERV 60
DB 130 FEAGAAAGAAPEEDLCAAFNVICNVGKDWRLARQLKVSQTKIDSIEDRYPRNLTERV 189

QY 61 RESLRWKNTKENATVAHLVGLRSCQNNLVADLVQEVQQAARDLQNRSGAMSPMS 116
DB 190 RESLRWKNTKENATVAHLVGLRSCQNNLVADLVQEVQQAARDLQNRSGAMSPMS 245

RESULT 8
US-10-207-655-418
Sequence 418, Application US/10207655
Publication No. US20030118592A1
GENERAL INFORMATION:
APPLICANT: Ledbetter, Jeffrey A.
APPLICANT: Hayden-Ledbetter, Martha S.
TITLE OF INVENTION: BINDING DOMAIN-IMMUNOGLOBULIN FUSION PROTEINS

```
; FILE REFERENCE: 390069.401C1
; CURRENT APPLICATION NUMBER: US/10/207,655
; CURRENT FILING DATE: 2002-07-25
; NUMBER OF SEQ ID NOS: 426
; SOFTWARE: Patent in version 3.0
; SEQ ID NO 418
; LENGTH: 210
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: fusion polypeptide
US-10-207-655-418

Query Match          64.5%; Score 382.5; DB 14; Length 210;
Best Local Similarity 61.7%; Pred. No. 3.8e-35;
Matches 71; Conservative 25; Mismatches 16; Indels 3; Gaps 1;

QY 1 FEAGAAAGAPGEEDLCAAFNVICDNYGKDWRLARQLKVSIDYPRNLTERVRSRLWKNTKENATVAHLVG 60
Db 87 FEAGTATAAPGEADLQVAFDVCNVGRDWKRLARELKVSEAKMDGIEEKYPRSLSERV 146

QY 61 RESLRWKNTKENATVAHLVGVALRSQCNMLVADLVQVQARDLQNRSGAMSPM 115
Db 147 RESLKWKNNAEKNASVAGLVKALRTCLNLVADLVVEAQES---VSKSENMSFV 198

RESULT 9
US-10-112-793-25
; Sequence 25, Application US/10112793
; Publication No. US20020192729A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; TITLE OF INVENTION: Apo-2 LI AND Apo-3 POLYPEPTIDES
; NUMBER OF SEQUENCES: 28
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/112,793
; FILING DATE: 28-Mar-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/828,683A
; FILING DATE: 31-Mar-1997
; APPLICATION NUMBER: 08/625328
; FILING DATE: 1-Apr-1996
; APPLICATION NUMBER: 08/710802
; FILING DATE: 23-Sep-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Marshchang, Diane L.
; REGISTRATION NUMBER: 35,600
; REFERENCE/DOCKET NUMBER: P1007P1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-5416
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 25:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 74 amino acids
; TYPE: AMINO ACID
; TOPOLOGY: Linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 25:
US-10-112-793-25

Query Match          64.4%; Score 382; DB 13; Length 74;
Best Local Similarity 100.0%; Pred. No. 1.1e-35;
Matches 74; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 23 ICDNVGKDWRLARQLKVSIDYPRNLTERVRSRLWKNTKENATVAHLVG 82
Db 1 ICDNVGKDWRLARQLKVSIDYPRNLTERVRSRLWKNTKENATVAHLVG 60

QY 83 ALRSQCNMLVADLV 96
Db 61 ALRSQCNMLVADLV 74

RESULT 10
US-10-287-594-5
; Sequence 5, Application US/10287594
; Publication No. US20030096288A1
; GENERAL INFORMATION:
; APPLICANT: Ni, Jian
; APPLICANT: Dixit, Vishva M
; TITLE OF INVENTION: RAIDD, A No. US20030096288A1el Death Adaptor Molecule
; FILE REFERENCE: 1488.0860002
; CURRENT APPLICATION NUMBER: US/10/287,594
; CURRENT FILING DATE: 2002-11-05
; PRIOR APPLICATION NUMBER: US/09/545,605
; PRIOR FILING DATE: 2001-04-07
; PRIOR APPLICATION NUMBER: 08/995,159
; PRIOR FILING DATE: 1997-12-19
; PRIOR APPLICATION NUMBER: 60,033,868
; PRIOR FILING DATE: 1996-12-20
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 5
; LENGTH: 74
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-287-594-5

Query Match          64.4%; Score 382; DB 14; Length 74;
Best Local Similarity 100.0%; Pred. No. 1.1e-35;
Matches 74; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 23 ICDNVGKDWRLARQLKVSIDYPRNLTERVRSRLWKNTKENATVAHLVG 82
Db 1 ICDNVGKDWRLARQLKVSIDYPRNLTERVRSRLWKNTKENATVAHLVG 60

QY 83 ALRSQCNMLVADLV 96
Db 61 ALRSQCNMLVADLV 74

RESULT 11
US-10-035-408-5
; Sequence 5, Application US/10035408
; Publication No. US20020123117A1
; GENERAL INFORMATION:
; APPLICANT: WALLACH, David
; APPLICANT: BOLDIN, Mark P.
; APPLICANT: VARFOLOMEEV, Eugene E.
; PANCER, Zeev
; METT, Igor
; GONCHAROV, Tanya M.
; WEINWURZEL, Henry
; TITLE OF INVENTION: MODULATORS OF REGULATORY PROTEINS
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BROWDY AND NEIMARK, P.L.L.C.
; STREET: 419 Seventh Street N.W., Ste. 300
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
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; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION NUMBER: US/10/035,408
; FILING DATE: 04-Jan-2002
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/894,626
; FILING DATE: 09-Dec-1997
; APPLICATION NUMBER: IL 112,742
; FILING DATE: 22-FEB-1995
; APPLICATION NUMBER: IL 115,289
; FILING DATE: 13-SEP-1995
; APPLICATION NUMBER: PCT/US96/02326
; FILING DATE: 15-FEB-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: BROWDY, Roger L.
; REGISTRATION NUMBER: 25,618
; REFERENCE/DOCKET NUMBER: WALLACH=17
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 628-5197
; TELEFAX: (202) 737-3528
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 62 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 5:
US-10-035-408-5

Query Match 53.6%; Score 318; DB 13; Length 62;
Best Local Similarity 100.0%; Pred.No.1.7e-28;
Matches 62; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 WRLARQLKVSPTKIDSDYPRNLTERRVRSRLRWKTEKENATVAHLVGLRSCQWN 60

QY 91 LV 92
Db 61 LV 62

RESULT 12
US-09-972-211-128
; Sequence 128, Application US/09972211
; Publication No. US20040048245A1
; GENERAL INFORMATION:
; APPLICANT: Shimkets, Richard A
; APPLICANT: Taupier Jr, Raymond J
; APPLICANT: Burgess, Catherine E
; APPLICANT: Zerhuseen, Bryan D
; APPLICANT: Mezes, Peter S
; APPLICANT: Rastelli, Luca
; APPLICANT: Malyankar, Uriel M
; APPLICANT: Grosse, William M
; APPLICANT: Alsobrook II, John P
; APPLICANT: Lepley, Denise M
; APPLICANT: Spytek, Kimberly Ann
; APPLICANT: Li, Li
; APPLICANT: Edinger, Shlomit
; APPLICANT: Gerlach, Valerie
; APPLICANT: Ellerman, Karen
; APPLICANT: MacDougall, John R
; APPLICANT: Gunther, Erik
; APPLICANT: Millet, Isabelle
; APPLICANT: Stone, David J
; APPLICANT: Smithson, Glennnda
; APPLICANT: Szekeres Jr, Edward S
; TITLE OF INVENTION: No. US20040048245A1el Human Proteins, Polynucleotides Encoding Th
; TITLE OF INVENTION: Methods Of Using The Same

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; FILE REFERENCE: 21402-141
; CURRENT APPLICATION NUMBER: US/09/972,211
; CURRENT FILING DATE: 2001-10-05
; PRIOR APPLICATION NUMBER: 60/238,325
; PRIOR FILING DATE: 2000-10-05
; PRIOR APPLICATION NUMBER: 60/238,323
; PRIOR FILING DATE: 2000-10-05
; PRIOR APPLICATION NUMBER: 60/238,400
; PRIOR FILING DATE: 2000-10-06
; PRIOR APPLICATION NUMBER: 60/238,397
; PRIOR FILING DATE: 2000-10-06
; PRIOR APPLICATION NUMBER: 60/238,401
; PRIOR FILING DATE: 2000-10-06
; PRIOR APPLICATION NUMBER: 60/238,379
; PRIOR FILING DATE: 2000-10-06
; PRIOR APPLICATION NUMBER: 60/238,402
; PRIOR FILING DATE: 2000-10-06
; PRIOR APPLICATION NUMBER: 30/238,384
; PRIOR FILING DATE: 2000-10-06
; PRIOR APPLICATION NUMBER: 60/238,373
; PRIOR FILING DATE: 2000-10-06
; PRIOR APPLICATION NUMBER: 60/238,372
; PRIOR FILING DATE: 2000-10-06
; PRIOR APPLICATION NUMBER: 60/238,383
; PRIOR FILING DATE: 2000-10-06
; PRIOR APPLICATION NUMBER: 60/238,382
; PRIOR FILING DATE: 2000-10-06
; PRIOR APPLICATION NUMBER: 60/275,892
; PRIOR FILING DATE: 2001-03-14
; PRIOR APPLICATION NUMBER: 60/296,860
; PRIOR FILING DATE: 2001-06-08
; NUMBER OF SEQ ID NOS: 198
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 128
; LENGTH: 95
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-972-211-128

Query Match 24.2%; Score 143.5; DB 11; Length 95;
Best Local Similarity 36.2%; Pred.No.2.2e-08;
Matches 34; Conservative 20; Mismatches 37; Indels 3; Gaps 1;

QY 4 GAAAGAAAGSEEDLCAPNVICDVGKWRRLARQLKVSPTKIDSDYPRNLTERRVRS 63
Db 3 GAASLTETREKLA---KLLDHLGLDGDWRELARKLGLSEADIDQIETESPRDLAEQSYQL 59

QY 64 LRIWKTEKENATVAHLVGLRSCQWNVLVDLVQ 97
Db 60 LRLWEQREGKNATLTGLTLEALRMGRDDAVELLR 93

RESULT 13
US-10-087-684-87
; Sequence 87, Application US/10087684
; Publication No. US20040029116A1
; GENERAL INFORMATION:
; APPLICANT: Edinger, Shlomit R.
; APPLICANT: MacDougall, John R.
; APPLICANT: Millet, Isabelle
; APPLICANT: Ellerman, Karen
; APPLICANT: Stone, David J.
; APPLICANT: Grosse, William M.
; APPLICANT: Lepley, Denise M.
; APPLICANT: Rieger, Daniel K.
; APPLICANT: Burgess, Catherine E.
; APPLICANT: Casman, Stacie, J.
; APPLICANT: Spytek, Kimberly A.
; APPLICANT: Boldog, Ferenc L.
; APPLICANT: Li, Li
; APPLICANT: Padigar, Muralidhara
; APPLICANT: Mishra, Vishnu
; APPLICANT: Shenoy, Suresh G.

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Wed Feb 16 07:33:25 2005

; PRIOR APPLICATION NUMBER: 09/972,211
; PRIOR FILING DATE: 2001-10-05
; PRIOR APPLICATION NUMBER: 60/238,325
; PRIOR FILING DATE: 2000-10-05
; PRIOR APPLICATION NUMBER: 60/238,323
; PRIOR FILING DATE: 2000-10-05
; PRIOR APPLICATION NUMBER: 60/238,400
; PRIOR FILING DATE: 2000-10-06
; PRIOR APPLICATION NUMBER: 60/238,397
; PRIOR FILING DATE: 2000-10-06
; PRIOR APPLICATION NUMBER: 60/238,401
; PRIOR FILING DATE: 2000-10-06
; PRIOR APPLICATION NUMBER: 60/238,379
; PRIOR FILING DATE: 2000-10-06
; PRIOR APPLICATION NUMBER: 60/238,402
; PRIOR FILING DATE: 2000-10-06
; PRIOR APPLICATION NUMBER: 30/238,384
; PRIOR FILING DATE: 2000-10-06
; PRIOR APPLICATION NUMBER: 60/238,373
; PRIOR FILING DATE: 2000-10-06
; PRIOR APPLICATION NUMBER: 60/238,372
; PRIOR FILING DATE: 2000-10-06
; PRIOR APPLICATION NUMBER: 60/238,383
; PRIOR FILING DATE: 2000-10-06
; PRIOR APPLICATION NUMBER: 60/238,382
; PRIOR FILING DATE: 2000-10-06
; PRIOR APPLICATION NUMBER: 60/275,892
; PRIOR FILING DATE: 2001-03-14
; PRIOR APPLICATION NUMBER: 60/296,860
; PRIOR FILING DATE: 2001-06-08
; NUMBER OF SEQ ID NOS: 200
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 128
; LENGTH: 95
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-096-625-128

Query Match	24.2%	Score 143.5;	DB 15;	Length 95;
Best Local Similarity	36.2%	Pred. No. 2.2e-08;		
Matches	34;	Conservative 20;	Mismatches 37;	Indels 3; Gaps 1;

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Db	3	GAASLTETREKLA---KLDDHDLGDDWRRLARQLKGLSEADIDQIETESPRDLAEQSYQL	59

Qy	64	LRIWKTEKENATVAHLVGLRSCQNNLVADLVQ	97
Db	60	LRLWEQREGKNATLGTLEALRKMGRRDDAVELLR	93

Search completed: February 11, 2005, 16:49:22
Job time : 374 secs

GenCore version 5.1.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: February 11, 2005, 16:41:39 ; Search time: 2065 Seconds
(without alignments)
8165.818 Million cell updates/sec

Title: US-09-824-134-1_COPY_388_735
Perfect score: 348
Sequence: 1 TTCGAGCGCGCGCGCGC.....GGGCCATGTCCCGATGCA 348

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 4708233 seqs, 24227607955 residues
Total number of hits satisfying chosen parameters: 9416466

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : GenEmbl.*

- 1: gb_ba.*
- 2: gb_hcg.*
- 3: gb_in.*
- 4: gb_om.*
- 5: gb_ov.*
- 6: gb_pat.*
- 7: gb_ph.*
- 8: gb_pl.*
- 9: gb_pr.*
- 10: gb_ro.*
- 11: gb_sts.*
- 12: gb_sy.*
- 13: gb_un.*
- 14: gb_vi.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	348	100.0	627	9	BT006927 Homo sapi
2	348	100.0	627	9	CP456738 Homo sapi
3	348	100.0	627	12	BT007629 Synthetic
4	348	100.0	1642	6	AR317240 Sequence
5	348	100.0	1642	6	AR380940 Sequence
6	348	100.0	1642	6	AR558975 Sequence
7	348	100.0	1642	6	AX774986 Sequence
8	348	100.0	1642	6	AX779974 Sequence
9	348	100.0	1642	9	HSU24231 Homo sapi
10	348	100.0	1642	9	HSU74301 Homo sapi
11	348	100.0	1701	6	AR211524 Sequence
12	348	100.0	1701	6	AR350946 Sequence
13	348	100.0	1701	9	HSMRNTX Homo sapi
14	348	100.0	1725	9	BC000334 Homo sapi
15	346.4	99.5	606	6	BD082771 Neuronal
16	344.8	99.1	606	6	BD082772 Neuronal
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18	307	88.2	456	6	CQ739366 Sequence
19	307	88.2	143409	2	AP001787 Homo sapi

20	307	88.2	169725	9	AP000879
21	294.2	84.5	66127	2	AC067995
22	195.2	56.1	847	4	AY725483
23	182.6	52.5	716	10	AF406779
24	182.6	52.5	1556	10	RNO441127
25	169.2	48.6	1377	10	MMU50406
26	169.2	48.6	1497	10	BC004584
27	169.2	48.6	1512	10	BC021400
28	167.6	48.2	618	10	MMU43184
29	159.2	45.7	222403	2	AC110851
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33	128.8	37.0	754	11	BV048738
34	81	23.3	570	5	AY555194
35	70.2	20.2	689	5	CR353855
36	70.2	20.2	779	5	BX932543
37	66.2	19.0	1575	5	BC082917
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ALIGNMENTS

BT006927 Homo sapiens Fas (TNFRSF6)-associated via death domain mRNA, complete cds.
BT006927 Homo sapiens (human)
BT006927.1 GI:30582692
FLI CDNA.
Homo sapiens (human)
Homo sapiens
Homo sapiens
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
Kalinine.N., Chen.X., Rolfs.A., Halleck.A., Hines.L., Eisenstein.S., Koundinya.M., Raphael.J., Moreira.D., Kelley.T., Labaer.J., Lin.Y., Phelan.M. and Farmer.A.
Cloning of human full-length CDSs in BD Creator(TM) System Donor vector
Unpublished
2 (bases 1 to 627)
Kalinine.N., Chen.X., Rolfs.A., Halleck.A., Hines.L., Eisenstein.S., Koundinya.M., Raphael.J., Moreira.D., Kelley.T., Labaer.J., Lin.Y., Phelan.M. and Farmer.A.
Direct Submission
Submitted (13-MAY-2003) BD Biosciences Clontech, 1020 East Meadow Circle, Palo Alto, CA 94303, USA
This CDS clone is a part of a collection of human full length expression clones generated by BD Biosciences Clontech and the Harvard Institute of Proteomics. Each CDS has been cloned in two forms: with and without stop-codon (to allow fusion with C-terminal tag). The CDS has been directionally cloned using BD In-Fusion(TM) cloning system between the Sali and HindIII sites of the pDNR-DUAL vector. Additional sequences in the clone: 'ACC' after Sali site and before 'ATG' to provide Kozak consensus sequence; 'GG' after last codon and before HindIII site to maintain reading frame.
Clone distribution: <http://bioinfo.clontech.com/orfclones>
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/clone="GH00418X1.0"

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/lab_host="DH5alpha T1 resistant"
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VICDNVKGWRRLARQLKVSVDKIDIEDRYPRNLTERVRESLRIRWNTKENATVAH
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ORIGIN

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Query Match      100.0%; Score 348; DB 9; Length 627;
Best Local Similarity 100.0%; Pred. No. 1.2e-81;
Matches 348; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTTCAGCGCGGGCGCGCGCGCGCGCGCGCTGGGGAAGAGACCTGTGTGACGCAATTT 60
DB 244 TTTCAGCGCGGGCGCGCGCGCGCGCGCGCTGGGGAAGAGACCTGTGTGACGCAATTT 303
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DB 304 AACGTCATATGTGATAATGTGGGAAAGATTGGAGAGCGTCTGCTCAGCTCAAAGTC 363
QY 121 TCAGACACCAAGATCGACAGCATCGACAGCAGATACCCCGCAACCTGACAGACGGTGTG 180
DB 364 TCAGACACCAAGATCGACAGCATCGACAGCAGATACCCCGCAACCTGACAGACGGTGTG 423
QY 181 CGGGAGTCACTGAGATCTGGAAGAACACAGAGAGGAGAGCAACAGAGTGGCCCACTG 240
DB 424 CGGGAGTCACTGAGATCTGGAAGAACACAGAGAGGAGAGCAACAGAGTGGCCCACTG 483
QY 241 GTGGGGGCTCTCAGTCTCTGCGAGATGAACCTGTGTGCTGACCTGGTACAGAGGTTTCAG 300
DB 484 GTGGGGGCTCTCAGTCTCTGCGAGATGAACCTGTGTGCTGACCTGGTACAGAGGTTTCAG 543
QY 301 CAGGCGCGTGACCTCCAGAACAGGAGTGGGGCCATGTCCCGATGTCA 348
DB 544 CAGGCGCGTGACCTCCAGAACAGGAGTGGGGCCATGTCCCGATGTCA 591

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RESULT 2

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CR456738
LOCUS      627 bp mRNA linear PRI 03-JUN-2004
DEFINITION Homo sapiens full open reading frame cDNA clone RZPD0834F046D for
            gene FADD, Fas (TNFRSF6)-associated via death domain; complete cds,
            incl. stopcodon.
ACCESSION  CR456738
VERSION    CR456738.1 GI:48145592
KEYWORDS   Full ORF shuttle clone, Gateway(TM), complete cds.
SOURCE     Homo sapiens (human)
ORGANISM   Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE  1 (bases 1 to 627)
AUTHORS   Ebert,L., Schick,M., Neubert,P., Schatten,R., Henze,S. and Korn,B.
TITLE     Cloning of human full open reading frames in Gateway(TM) system
          entry vector (pDONR201)
JOURNAL   Unpublished
REFERENCE  2 (bases 1 to 627)
AUTHORS   Ebert,L., Schick,M., Neubert,P., Schatten,R., Henze,S. and Korn,B.
TITLE     Direct Submission
JOURNAL   Submitted (03-JUN-2004) RZPD Deutsches Ressourcenzentrum fuer
          Genomforschung GmbH, Im Neuenheimer Feld 580, D-69120 Heidelberg,
          Germany
COMMENT   RZPD; RZPD0834F046D, ORFNO 788
          www.rzpd.de/cgi-bin/products/cl.cgi?CloneID=RZPD0834F046D RZPDLIB;
          Human Full ORF Clones Gateway(TM) - RZPD (kan-resist.) RZPD LIB No.
          834
          www.rzpd.de/cgi-bin/products/showLib.pl.cgi/response?libNo=834

```

```

www.rzpd.de/products/orfclones/
Contact: Inge Arlt
RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH,
Heubnerweg 6, D-14059 Berlin, Germany
Tel: +49 30 32639 100
Fax: +49 30 32639 111
www.rzpd.de

```

This clone is available from RZPD; contact RZPD (customer.service@rzpd.de) for further information. This CDS clone is a part of a collection of human full length expression clones generated by RZPD. This CDS has been cloned incl. stopcodon. This CDS has been inserted into pDONR201 via a BP Clonase(TM) reaction. Additional sequence has been added in front of the start codon: att. .AAAAA GCA GGC (ATG). The last base of the last coding triplet has been changed to T, which might lead to an amino acid change at the C terminus of the polypeptide. The stop codon has been set to TAA followed by TTAACCCAGCTTCTT. att. Compared to the reference sequence NM_003824 we did not find any amino acid exchanges. Clone distribution: <http://www.rzpd.de/products/orfclones/>.

FEATURES

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            /db_xref="taxon:9606"
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            /note="Vector: pDONR201, Site_1: attP1; Site_2: attP2"
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            /gene="FADD"
            /codon_start=1
            /protein_id="CAG33019.1"
            /db_xref="GI:48145593"
            /translation="MDPFLVLLHSVSSLSSELTTELKFLCLGRVGRKRLVQSGLD
            LFSMLLEQNDLEPGHTELLRELLRLRRVDDFEAGAAAGAPGEDLCAAFN
            VICDNVKGWRRLARQLKVSVDKIDIEDRYPRNLTERVRESLRIRWNTKENATVAH
            LVGALRSCOMNLVADLVQEVQVQARDLQNRSGAMSPMWSNDSASTSEAS"

```

ORIGIN

```

Query Match      100.0%; Score 348; DB 9; Length 627;
Best Local Similarity 100.0%; Pred. No. 1.2e-81;
Matches 348; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTTCAGCGCGGGCGCGCGCGCGCGCGCGCTGGGGAAGAGACCTGTGTGACGCAATTT 60
DB 244 TTTCAGCGCGGGCGCGCGCGCGCGCGCGCTGGGGAAGAGACCTGTGTGACGCAATTT 303
QY 61 AACGTCATATGTGATAATGTGGGAAAGATTGGAGAGCGTCTGCTCAGCTCAAAGTC 120
DB 304 AACGTCATATGTGATAATGTGGGAAAGATTGGAGAGCGTCTGCTCAGCTCAAAGTC 363
QY 121 TCAGACACCAAGATCGACAGCATCGACAGCAGATACCCCGCAACCTGACAGACGGTGTG 180
DB 364 TCAGACACCAAGATCGACAGCATCGACAGCAGATACCCCGCAACCTGACAGACGGTGTG 423
QY 181 CGGGAGTCACTGAGATCTGGAAGAACACAGAGAGGAGAGCAACAGAGTGGCCCACTG 240
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JOURNAL
Submitted (06-APR-1995) Arul M. Chinnaiyan, Pathology, University
of Michigan, 1150 W. Medical Center Drive, Ann Arbor, MI 48109, USA

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CDS

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Matches 348; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 493 TCAGACACAAGATCGACAGCATCGAGGACAGATACCCCCGACCTTGACAGAGCGGTG 552
QY 181 CGGGAGTCACTGAGTAATCTGGAAGAACACAGAGAGGAGAACGCAACAGTGGCCACCTG 240
DB 553 CGGGAGTCACTGAGTAATCTGGAAGAACACAGAGAGGAGAACGCAACAGTGGCCACCTG 612
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DB 613 GTGGGGGCTCTCAGGTCCTCGCACATGAACCTGGTGGCTGACCTGGTACAGAGGTTTCAG 672
QY 301 CAGGCCCGTGACTCCAGAACAGGAGTGGGGCCATGTCCCAGATGTCA 348
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Keywords
Source
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1642 bp DNA linear
PRI 30-SEP-2002

REFERENCE
AUTHORS
TITLE
JOURNAL
MEDLINE
PUBMED
REFERENCE
AUTHORS
TITLE
JOURNAL
Medline
PUBMED
Direct Submission
Submitted (13-OCT-1996) LGT, NCHGR, NIH, RM 3B07 Bldg. 49, 49
Convent Dr., Bethesda, MD 20892-4442, USA
Location/Qualifiers

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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE
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Medline
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Direct Submission
Submitted (02-FEB-1996)
Human Fas-associated protein containing protein mRNA,
complete cds.
1642 bp mRNA linear
PRI 02-FEB-1996

HSU24231
LOCUS
DEFINITION
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Version
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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TITLE
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Authors
Title
Journal
Medline
PUBMED
Direct Submission
Submitted (02-FEB-1996)
Human Fas-associated protein containing protein mRNA,
complete cds.
1642 bp mRNA linear
PRI 02-FEB-1996

HSU24231

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Best Local Similarity 100.0%; Pred. No. 1.2e-81;
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LOCUS      1701 bp      DNA      linear      PAT 20-JUN-2002
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ACCESSION AR211524
VERSION    AR211524.1 GI:21514868
KEYWORDS
SOURCE     Unknown.
ORGANISM   Unclassified.
REFERENCE  1 (bases 1 to 1701)
AUTHORS    Wallach,D., Boldin,M., Goncharov,T. and Golstev,Y.V.
TITLE      Modulators of the function of FAS receptors and other proteins
JOURNAL    Patent: US 6399327-A 1 04-JUN-2002;
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QY 61 AACGTCATATGTGATAATGTGGGAAAGATTGGAGAAGGCTGCTCGCTCAAGTC 120
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DB 448 AACGTCATATGTGATAATGTGGGAAAGATTGGAGAAGGCTGCTCGCTCAAGTC 507
QY 121 TCAGACACCAAGATCGACAGCATCGAGACAGATACCCCGCAACCTGCAGACGCTGTG 180
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DB 508 TCAGACACCAAGATCGACAGCATCGAGACAGATACCCCGCAACCTGCAGACGCTGTG 567
QY 181 CGGGAGTCACTGAGATCTCGAAGAACACAGAGAGGAGAACGCAACAGTGGCCACCTG 240
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QY 241 GTGGGGGCTCTCAGTCTCGCAGATGAACCTGGTGGCTGACCTGGTACAGAGGTTTCAG 300
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QY 301 CAGGCGCGGTGACCTCCAGAACAGGAGTGGGGCCATGTCCCGCATGTCA 348
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VERSION    AR350946.1 GI:33752607
KEYWORDS
SOURCE     Unknown.
ORGANISM   Unclassified.
REFERENCE  1 (bases 1 to 1701)
AUTHORS    Wallach,D., Boldin,M., Goncharov,T. and Golstev,Y.V.
TITLE      Modulators of the function of FAS receptors and other proteins
JOURNAL    Patent: US 6586571-A 1 01-JUL-2003;
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Best Local Similarity 100.0%; Pred. No. 1.2e-81;
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DB 388 TTCGAGCGGGCGCGCGCGCGCGCTGGGGAAGAGACCTGTGTGCAGCATTT 447
QY 61 AACGTCATATGTGATAATGTGGGAAAGATTGGAGAAGGCTGCTCGCTCAAGTC 120
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QY 121 TCAGACACCAAGATCGACAGCATCGAGACAGATACCCCGCAACCTGCAGACGCTGTG 180
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DB 508 TCAGACACCAAGATCGACAGCATCGAGACAGATACCCCGCAACCTGCAGACGCTGTG 567
QY 181 CGGGAGTCACTGAGATCTCGAAGAACACAGAGAGGAGAACGCAACAGTGGCCACCTG 240
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DEFINITION	BD082771	BD082771	Neuronal MOR1 isoforms.				
ACCESSION	BD082771	BD082771	Neuronal MOR1 isoforms.				
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REFERENCE	Bingham,B.W., Young,K.H., Timothy,A., Wood and Birsan,C.	Bingham,B.W., Young,K.H., Timothy,A., Wood and Birsan,C.	Bingham,B.W., Young,K.H., Timothy,A., Wood and Birsan,C.				
AUTHORS	Neuronal MOR1 isoforms	Neuronal MOR1 isoforms	Neuronal MOR1 isoforms				
TITLE	Patent: JP 2001522247-A	Patent: JP 2001522247-A	Patent: JP 2001522247-A				
JOURNAL	1 13-NOV-2001;	1 13-NOV-2001;	1 13-NOV-2001;				

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